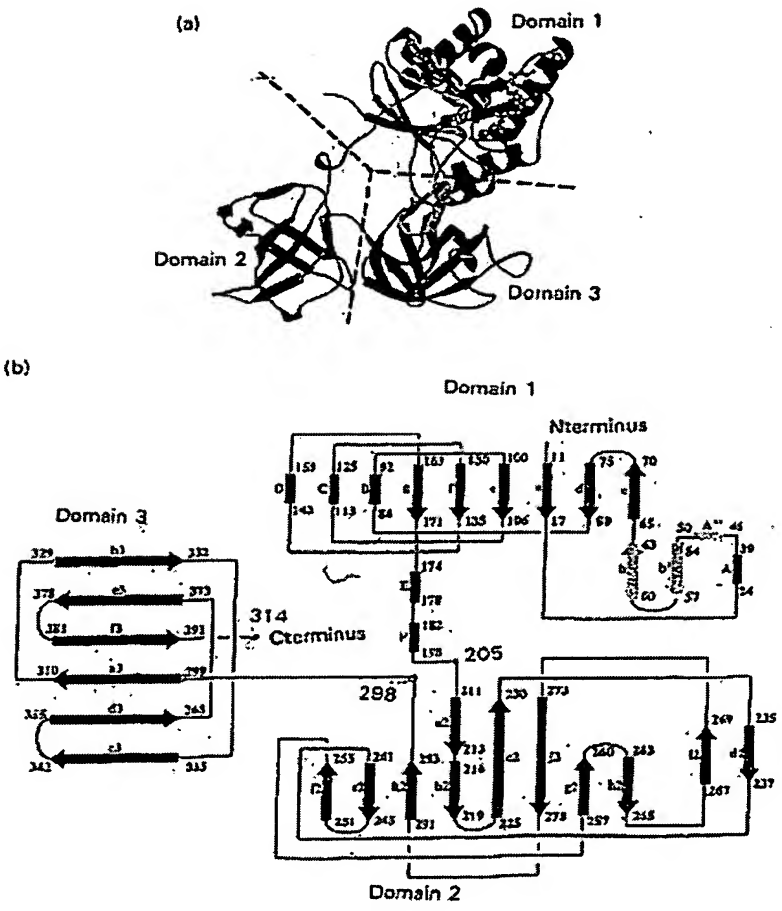
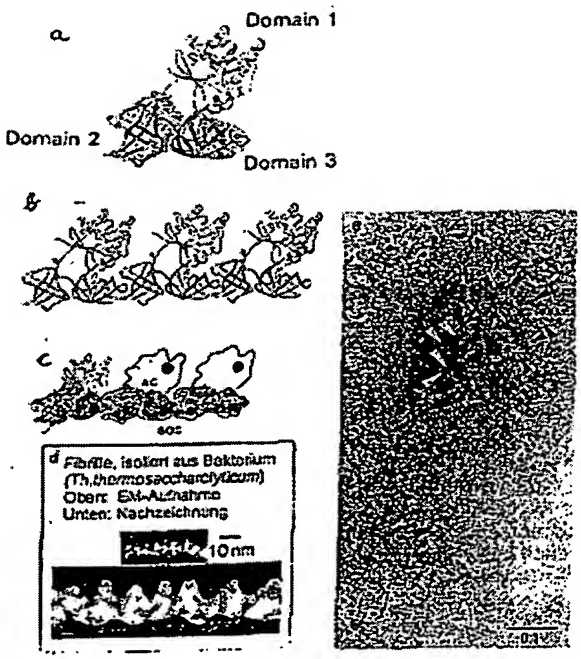
Figur 1



[Key to Figure 1:]

Figur = Figure

Figur 2



[Key to Figure 2:]

Figur = Figure

Fibrille, isoliert aus Bakterium = Fibrilla, isolated from the bacterium

Oben: EM-Aufnahme = Above: EM image

Unten: Nachzeichnung = Below: Copy

Fig. 3

(a1)
Vektor pEGFP (Clontech):

```
          BsrGI       STOP                        EcoRI
GAC GAG CTG TAC AAG TAA AGC GGC CGC GAC TCT AGA ATT CCA
CTG CTC GAC ATG TTC ATT TCG CCG GCG CTG AGA TCT TAA GGT
```

BsrGI-Schnittstelle:

```
  T   GTACA
  ACATG   T
```

EcoRI-Schnittstelle:

```
    G   AATTC
    CTTAA   G
```

Synthetisch hergestelltes Oligonukleotid zur Einklonierung des His-Tags in den Vektor:

```
5'BsrGI                                          BsrGI       EcoRI 3'
G TAC AAG CTT CAT CAC CAT CAC CAT CAC TAA CTG TAC AAG TAAG
      TTC GAA GTA GTG GTA GTG GTA GTG ATT GAC ATG TTC ATTCTTAA
3'                                                              5'
  Tyr-Lys-Leu-His-His-His-His-His-His-STOP-
```

Ergebnis: pEGFP(His)

(a2)

Vektor pEGFP(His):

```
GCC TGC AGG -%- ACC ATG GTG
CGG ACG TCC -%- TGG TAC CAC
```

PstI-Schnittstelle:

```
CTGCA    G
G    ACGTC
```

NcoI-Schnittstelle:

```
C    CATGG
GGTAC    C
```

Fusionsstellen zum EF-Tu-Gen:

```
                Start EF-Tu                                  Start EGFP
5'    PstI                                  HindIII    NcoI        3'
ACT AGC TGC AGC ATG TCT AAA -%- CTG GGC AAG CTT ACC ATG GTG
TGA TCG ACG TCG TAC AGA TTT -%- GAC CCG TTC GAA TGG TAC CAC
3'                                                            5'
Thr-Ser-Cys-Ser-Met-Ser-Lys-----Leu-Gly-Lys-Leu- Thr-Met-Val
```

[Key to Figure 3:]

Vektor = Vector

Schnittstelle = Interface

Synthetisch hergestelltes Oligonukleotid zur Einklonierung des His-Tags in den Vektor =

Synthetically produced oligonucleotide for cloning the His tag in the vector

Ergebnis = Result

Fusionsstellen zum EF-Tu-Gen = Fusion points in the EF-Tu gene

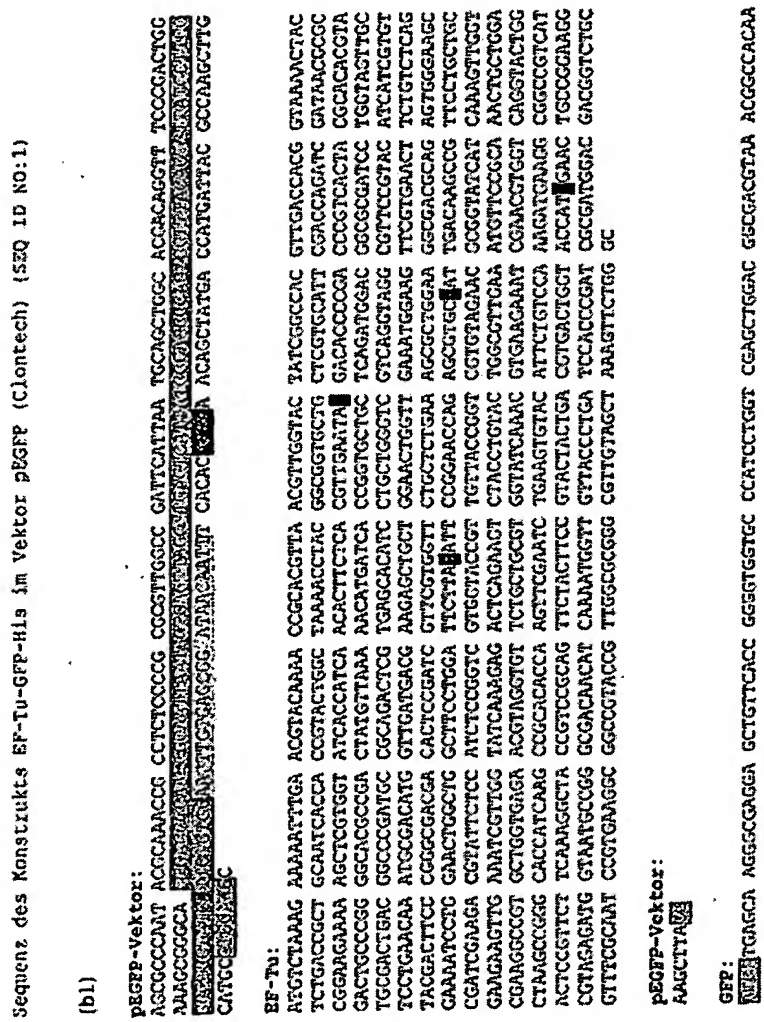
(a3)

Fusionsstellen zur Domäne 3:

```
5'     PstI                                  Cys  HindIII     NcoI   3'
ACT AGC TGC AGC GCT AAG CCG -$- CTG GGC TGC AAG CTT ACC ATG GTG
TGA TCG ACG TCG CGA TTC GGC -$- GAC CCG ACG TTC GAA TGG TAC CAC
3''                                                              5'
Thr-Ser-Cys-Ser-Ala-Lys-Pro-----Leu-Gly-Cys-Lys-Leu-Thr-Met-Val
```

[Key to 4/15:]

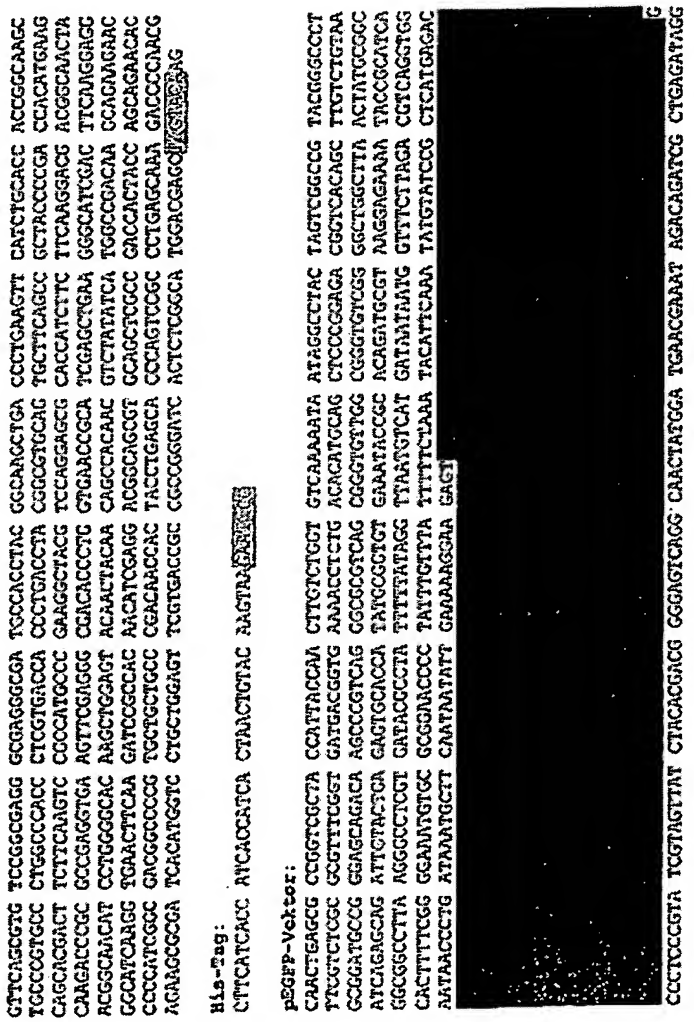
Fusionsstellen zum Domäne 3 = Fusion points in domain 3



[Key to 5/15:]

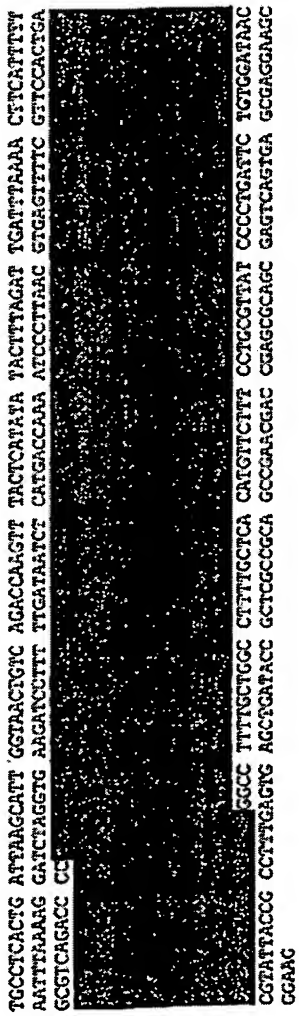
Sequenz des Konstrukts EF-Tu-GFP-His im Vektor pEGFP = Sequence of the construct EF-Tu-GFP-His in the vector pEGFP

Vektor = Vector



[Key to 6/15:]

Vektor = Vector



[Key to 7/15:]

Sequenz: Lac-Promotor = Sequence: Lac-promoter

Ribosomen-Bindungsstelle = Ribosome binding site

Ampicillin-Resistenz-Gen = Ampicillin resistance gene

Klonierungsstellen = Cloning sites

The sequence contains four silent mutations ( ) that are clearly present according to sequence analysis:

(1) To be: TAT, Is: TA -> Tyr; codon usage (entire E. coli genome) is changed from 16.2 to 12.2

(2) To be: TAC, Is: TA -> Tyr; codon usage (entire E. coli genome) is changed from 12.2 to 16.2

(3) To be: GCA, Is: GC -> Ala; codon usage (entire E. coli genome) is changed from 20.1 to 33.6

(4) To be: ATT, Is: AT -> Ile; codon usage (entire E. coli genome) is changed from 30.3 to 25.1 (frequency per thousand)

Sequenz des Konstrukts Domäne 3 von EF-Tu-GFP-His im Vektor pEGFP (Clontech) (SEQ ID NO:2)
(b2)

pEGFP-Vektor:
AGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCATTAA TGCAGCTGGC ACGACAGGTT TCCCGACTGG
AAAGCGGGCA [illegible]
[illegible]
CATGC[illegible]C

Domäne 3 von EF-Tu:
GCTAAGCCGG GCACCATCAA GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG GCGGCCGTCA
TACTCCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC CGTACTACTG ACGTGACTGG TACCAT[illegible]GAA CTGCCGGAAG
GCGTAGAGAT GGTAATGCCG GGCGACAACA TCAAAATGGT TGTTACCCTG ATCCACCCGA TCGCGATGGA CGACGGTCTG
CGTTTCGCAA TCCGTGAAGG CGGCCGTACC GTTGGCGCGG GCGTTGTAGC TAAAGTTCTG GGCTGC

pEGFP-Vektor:
AAGCTTA[illegible]

GFP:
[illegible]TGAGCA AGGGCGAGGA GCTGTTCACC GGGGTGGTGC CCATCCTGGT CGAGCTGGAC GGCGACGTAA ACGGCCACAA
GTTCAGCGTG TCCGGCGAGG GCGAGGGCGA TGCCACCTAC GGCAAGCTGA CCCTGAAGTT CATCTGCACC ACCGGCAAGC
TGCCCGTGCC CTGGCCCACC CTCGTGACCA CCCTGACCTA CGGCGTGCAG TGCTTCAGCC GCTACCCCGA CCACATGAAG
CAGCACGACT TCTTCAAGTC CGCCATGCCC GAAGGCTACG TCCAGGAGCG CACCATCTTC TTCAAGGACG ACGGCAACTA
CAAGACCCGC GCCGAGGTGA AGTTCGAGGG CGACACCCTG GTGAACCGCA TCGAGCTGAA GGGCATCGAC TTCAAGGAGG
ACGGCAACAT CCTGGGGCAC AAGCTGGAGT ACAACTACAA CAGCCACAAC GTCTATATCA TGGCCGACAA GCAGAAGAAC
GGCATCAAGG TGAACTTCAA GATCCGCCAC AACATCGAGG ACGGCAGCGT GCAGCTCGCC GACCACTACC AGCAGAACAC
CCCCATCGGC GACGGCCCCG TGCTGCTGCC CGACAACCAC TACCTGAGCA CCCAGTCCGC CCTGAGCAAA GACCCCAACG
AGAAGCGCGA TCACATGGTC CTGCTGGAGT TCGTGACCGC CGCCGGGATC ACTCTCGGCA TGGACGAGC[illegible]AG

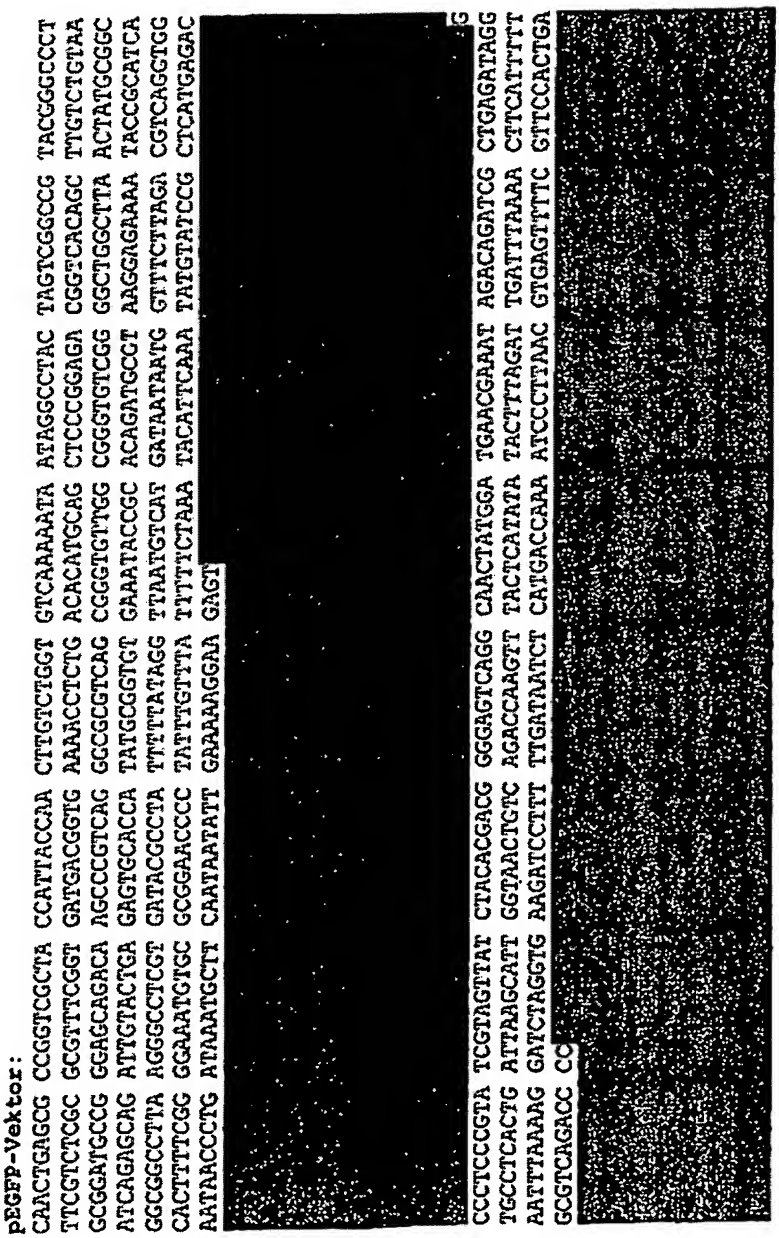
His-Tag:
CTTCATCACC ATCACCATCA CTAACTGTAC AAGTAA[illegible]CG

[Key to 9/15:]

Sequenz des Konstrukts Domäne 3 von EF-Tu-GFP-His im Vektor pEGFP (Clontech) (SEQ ID No: 2) (b2) = Sequence of the domain-3 construct of EF-Tu-GFP-His in the vector pEGFP (Clontech) (SEQ ID No: 2) (b2)

Vektor = Vector

Domäne = Domain


pEGFP-Vektor:
CAACTGAGCG CCGGTCGCTA CCATTACCAA CTTGTCTGGT GTCAAAAATA ATAGGCCTAC TAGTCGGCCG TACGGCCCT
TTCGTCTCGC GCGTTTCGGT GATGACGGTG AAAACCTCTG ACACATGCAG CTCCCGGAGA CGGTCACAGC TTGTCTGTAA
GCGGATGCCG GGAGCAGACA AGCCCGTCAG GGCGCGTCAG CGGGTGTTGG CGGGTGTCGG GGCTGGCTTA ACTATGCGGC
ATCAGAGCAG ATTGTACTGA GAGTGCACCA TATGCGGTGT GAAATACCGC ACAGATGCGT AAGGAGAAAA TACCGCATCA
GGCGGCCTTA AGGGCCTCGT GATACGCCTA TTTTTATAGG TTAATGTCAT GATAATAATG GTTTCTTAGA CGTCAGGTGG
CACTTTTCGG GGAAATGTGC GCGGAACCCC TATTTGTTTA TTTTTCTAAA TACATTCAAA TATGTATCCG CTCATGAGAC
AATAACCCTG ATAAATGCTT CAATAATATT GAAAAAGGAA GAGT
CCCTCCCGTA TCGTAGTTAT CTACACGACG GGGAGTCAGG CAACTATGGA TGAACGAAAT AGACAGATCG CTGAGATAGG
TGCCTCACTG ATTAAGCATT GGTAACTGTC AGACCAAGTT TACTCATATA TACTTTAGAT TGATTTAAAA CTTCATTTTT
AATTTAAAAG GATCTAGGTG AAGATCCTTT TTGATAATCT CATGACCAAA ATCCCTTAAC GTGAGTTTTC GTTCCACTGA
GCGTCAGACC CC

[Key to 10/15:]

Vektor = Vector

[redacted]GGCC TTTTGCTGGC CTTTTGCTCA CATGTTCTTT CCTGCGTTAT CCCCTGATTC TGTGGATAAC
CGTATTACCG CCTTTGAGTG AGCTGATACC GCTCGCCGCA GCCGAACGAC CGAGCGCAGC GAGTCAGTGA GCGAGGAAGC
GGAAG

[redacted] Lac-Promotor

[redacted] Lac-Operator

[redacted] Ribosomen-Bindungsstelle

[redacted] Ampicillin-Resistenz-Gen

[redacted] pUC Plasmid-Replications-Origin

[redacted]
5. [redacted] PstI
6. [redacted] NcoI
7. [redacted] BsrGI
8. [redacted] EcoRI

Die Sequenz enthält eine silent mutation ([redacted]), die laut Sequenzanalyse eindeutig vorhanden ist:

Soll: ATT, Ist: ATC -> Ile; Codon usage (gesamtes Genom E. coli) ändert sich von 30,3 zu 25,1 (Frequenz pro Tausend)

[Key to 11/15:]

Sequenz: Lac-Promotor = Sequence: Lac-promoter

Ribosomen-Bindungsstelle = Ribosome binding site

Ampicillin-Resistenz-Gen = Ampicillin resistance gene

Klonierungsstellen = Cloning Sites

[last sentence:] The sequence contains a silent mutation ( ), which is clearly present according to the sequence analysis:

To be: ATT, Is: AT -> Ile; codon usage (entire E. coli genome) is changed from 30.3 to 25.1 (frequency per thousand)

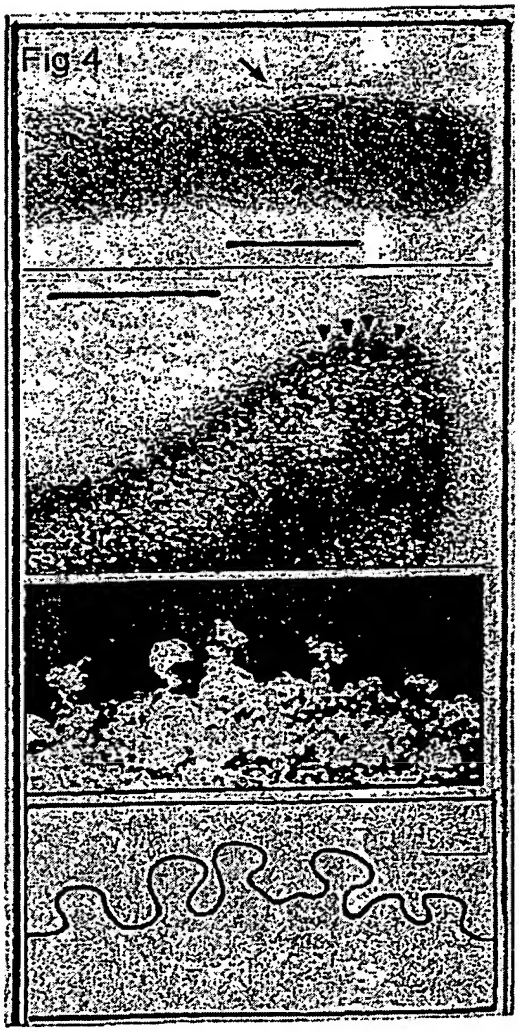


Fig 4

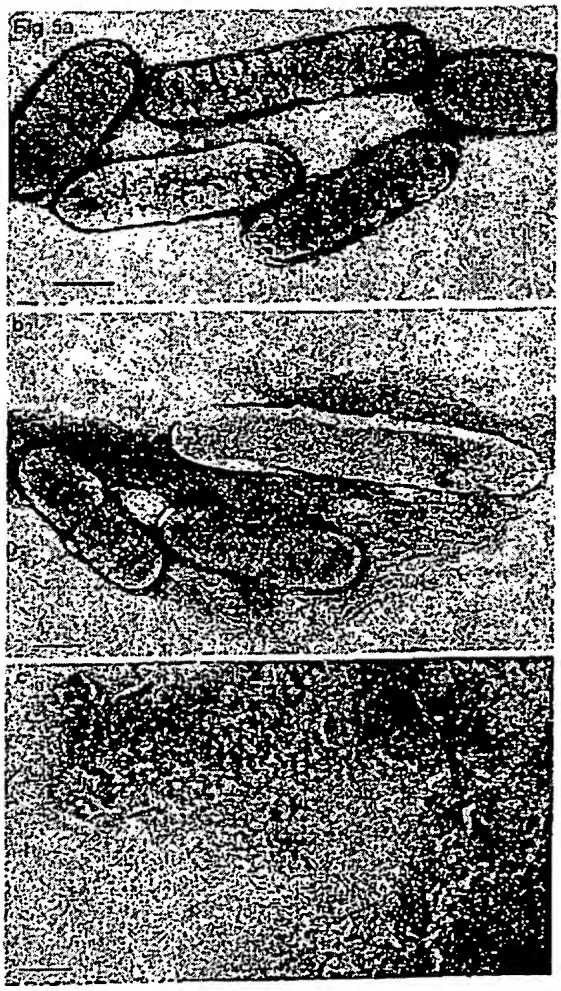


Fig 5a
b
c

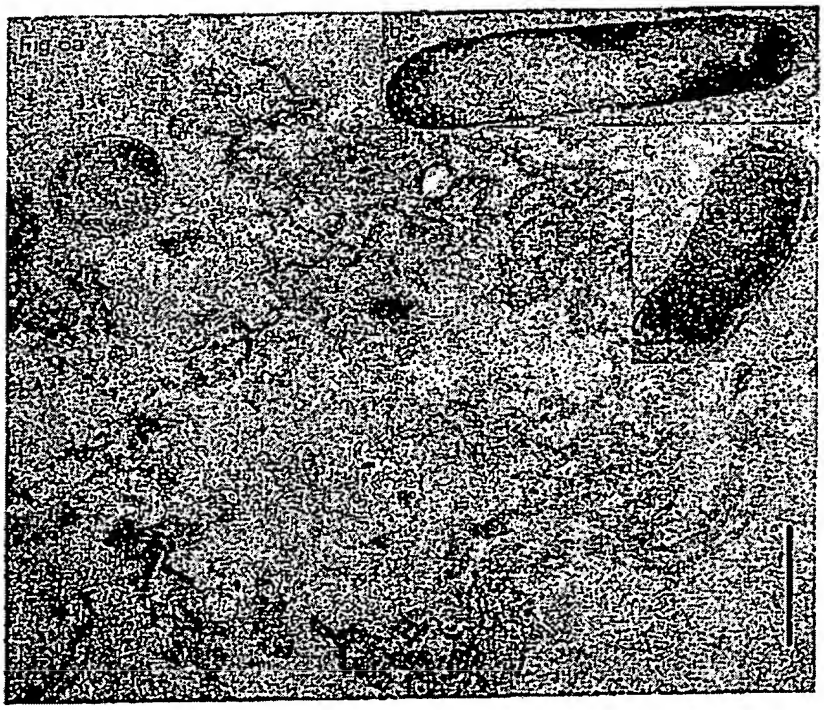
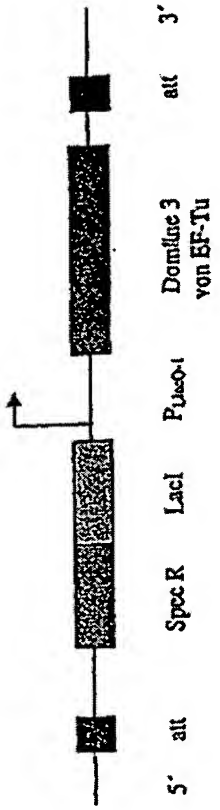


fig 6a



Figur 7

[Key to Figure 7:]

Figur = Figure

Domäne 3 von EF-Tu = Domain 3 of EF-Tu